

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/702,525DATE: 01/12/98
TIME: 12:00:15

INPUT SET: S22465.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Sharpe, Sharpe
Borriello, Francescopaolo
Freeman, Gordon
Nadler, Lee

(ii) TITLE OF INVENTION: Novel Forms of T Cell Costimulatory
Molecules and Uses Therefor

(iii) NUMBER OF SEQUENCES: 65

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD
(B) STREET: 28 State Street
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02109-1875

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/205,697
(B) FILING DATE: 02-Mar-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mandragouras, Amy E.
(B) REGISTRATION NUMBER: 36,207
(C) REFERENCE/DOCKET NUMBER: BWI-120CPUS

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617)227-7400
(B) TELEFAX: (617)227-5941

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47
48 (2) INFORMATION FOR SEQ ID NO:1:
49
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 1888 base pairs
52
53 (B) TYPE: nucleic acid
54 (C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear
56
57 (ii) MOLECULE TYPE: cDNA
58
59 (ix) FEATURE:
60 (A) NAME/KEY: CDS
61 (B) LOCATION: 249..1208
62
63 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
64
65
66 GAGTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACCTCAACC 60
67
68 TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120
69
70 TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTGTG GAGCCTAGGA 180
71
72 GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 240
73
74 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC 290
75 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
76 1 5 10
77
78 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT 338
79 Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
80 15 20 25 30
81
82 CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG 386
83 Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val
84 35 40 45
85
86 AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT 434
87 Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp
88 50 55 60
89
90 GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG 482
91 Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu
92 65 70 75
93
94 TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG 530
95 Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg
96 80 85 90
97
98 ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC 578
99 Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val

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100	95	100	105	110	
101					
102	CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA				626
103	Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg				
104		115	120	125	
105					
106	GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA				674
107	Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys				
108		130	135	140	
109					
110					
111	GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG TCT GGA AAC CCA TCT GCA				722
112	Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala				
113		145	150	155	
114					
115	GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC GGG GGT TTC CCA AAG CCT				770
116	Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro				
117		160	165	170	
118					
119	CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA TTA CCT GGC ATC AAT ACG				818
120	Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr				
121		175	180	185	190
122					
123	ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG TAC ACC ATT AGT AGC CAA				866
124	Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln				
125		195	200	205	
126					
127	CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC ATT AAG TGT CTC ATT AAA				914
128	Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys				
129		210	215	220	
130					
131	TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC ACC TGG GAA AAA CCC CCA				962
132	Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro				
133		225	230	235	
134					
135	GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG GCA GGA				1010
136	Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly				
137		240	245	250	
138					
139	TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC ATC AAA TGC				1058
140	Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys				
141		255	260	265	270
142					
143	TTC TGT AAG CAC GGT CTC ATC TAC CAT TTG CAA CTG ACC TCT TCT GCA				1106
144	Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala				
145		275	280	285	
146					
147	AAG GAC TTC AGA AAC CTA GCA CTA CCC TGG CTC TGC AAA CAC GGT TCT				1154
148	Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser				
149		290	295	300	
150					
151	CTA GGT GAA GCC TCT GCA GTG ATT TGC AGA AGT ACT CAG ACG AAT GAA				1202
152	Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu				

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153          305          310          315
154
155 CCA CAG TAGTTCTGCT GTTTCTGAGG ACGTAGTTTA GAGACTGAAT TCTTTGGAAA      1258
156 Pro Gln
157     320
158
159 GGACATAGGG ACAGTTTGCA CATTGCTTG CACATCACAC ACACACACAC ACACACACAC      1318
160
161 ACACACACAC ACACACACAC ACACACACAC ACACACACAC TCTCTCTCTC TCTCTCTCTC      1378
162
163 GATACCTTAG GATAGGGTTC TACCCTGTTG CTCAGTGACA AAGAATCACT CTGTGGCGGA      1438
164
165 GGCAGGCTTC AAGCTTGCAG CAATCCTCCT GCACCAGTTT CCTGAGTGCC AGACTTCCAG      1498
166
167 GTGTAAGCTA TGGCACTTAG CAGAACACTA GCTGAATCAA TGAAGACACT GAGGTTCCAA      1558
168
169 GAGGGAACCT GAATTATGAA GGTGAGTCAG AATCCAGATT TCCTGGCTCT ACCACTCTTA      1618
170
171 ACCTGTATCT GTTAGACCCC AAGCTCTGAG CTCATAGACA AGCTAATTTA AAATGCTTTT      1678
172
173 TAATAAGCAG AAGGCTCAGT TAGTACGGGG TTCAGGATAC TGCTTACTGG CAATATTTGA      1738
174
175 CTAGCCTCTA TTTTGTTTGT TTTTAAAGG CCTACTGACT GTAGTGTAAT TTGTAGGAAA      1798
176
177 CATGTTGCTA TGTATACCCA TTTGAGGGTA ATAAAAATGT TGGTAATTTT CAGCCAGCAC      1858
178
179 TTTCCAGGTA TTTCCCTTTT TATCCTTCAT      1888
180
181

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

193 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
194   1             5             10             15
195
196 Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
197           20           25           30
198
199 Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
200       35           40           45
201
202 Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
203     50           55           60
204
205 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val

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	65		70		75		80
206							
207							
208	Ile	Ala	Gly	Lys	Leu	Lys	Val
209				85			90
210							95
211	Tyr	Asp	Asn	Thr	Thr	Tyr	Ser
212				100			105
213							110
214	Asp	Arg	Gly	Thr	Tyr	Ser	Cys
215				115			120
216							125
217	Tyr	Glu	Val	Lys	His	Leu	Ala
218				130			135
219							140
220	Phe	Ser	Thr	Pro	Asn	Ile	Thr
221				145			150
222							155
223	Lys	Arg	Ile	Thr	Cys	Phe	Ala
224				165			170
225							175
226	Ser	Trp	Leu	Glu	Asn	Gly	Arg
227				180			185
228							190
229	Ser	Gln	Asp	Pro	Glu	Ser	Glu
230				195			200
231							205
232	Phe	Asn	Thr	Thr	Arg	Asn	His
233				210			215
234							220
235	Asp	Ala	His	Val	Ser	Glu	Asp
236				225			230
237							235
238							240
239	Pro	Pro	Asp	Ser	Lys	Asn	Thr
240				245			250
241							255
242	Ala	Val	Ile	Thr	Val	Val	Val
243				260			265
244							270
245	Lys	His	Gly	Leu	Ile	Tyr	His
246				275			280
247							285
248	Phe	Arg	Asn	Leu	Ala	Leu	Pro
249				290			295
250							300
251	Glu	Ala	Ser	Ala	Val	Ile	Cys
252				305			310
253							315
254							320

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2516 base pairs

INPUT SET: S22465.raw

***** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

3001 (2) INFORMATION FOR SEQ ID NO:65:

3002

3003 (i) SEQUENCE CHARACTERISTICS:

3004 (A) LENGTH: 226 amino acids

3005 (B) TYPE: amino acid

3006 (D) TOPOLOGY: linear

3007

3008 (ii) MOLECULE TYPE: protein

3009

3010 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

3011

3012 Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe

3013 1 5 10 15

3014

3015 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser

3016 20 25 30

3017

3018 Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp

3019 35 40 45

3020

3021 Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser

3022 50 55 60

3023

3024 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val

3025 65 70 75 80

3026

3027 Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu

3028 85 90 95

3029

3030 Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser

3031 100 105 110

3032

3033 Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr

3034 115 120 125

3035

3036 Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Pro Pro

3037 130 135 140

3038

3039 Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly

3040 145 150 155 160

3041

3042 Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys

3043 165 170 175

3044

3045 Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala

3046 180 185 190

3047

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3048 Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser
3049 195 200 205
3050
3051 Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu
3052 210 215 220
3053
3054 Pro Gln
3055 225
3056
3057
3058
3059
3060
3061
3062

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/702,525

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Line

Error

Original Text